

Amendments to the Claims

Please cancel claim 12 without prejudice. Please amend the remaining claims as shown below in the List of Claims.

List of Claims

1-10. Cancelled.

11. (Currently amended) A process for producing an L-amino acid comprising:

- a) culturing ~~a modified~~ an enterobacterium of the genus *Escherichia* in a medium for a time and under conditions suitable for producing said L-amino acid; and
- b) recovering or isolating said L-amino acid;

wherein the *yjgF* open reading frame of said ~~modified~~ enterobacterium has been inactivated by one or more methods of mutagenesis selected from the group consisting of: deletion of all or part of the *yjgF* open reading frame; insertional mutagenesis due to homologous recombination; and transitional or transversional mutagenesis with incorporation of a non-sense mutation in the *yjgF* open reading frame; and

wherein said *yjgF* open reading frame is ~~obtainable from *Escherichia* by PCR amplification using primer yjgF-1 (SEQ ID NO: 3) and primer yjgF-4 (SEQ ID NO: 6)~~ encodes the polypeptide of SEQ ID NO:2.

12. Cancelled.

13. (Previously presented) The process of claim 11, wherein said *yjgF* open reading frame has the nucleotide sequence of SEQ ID NO:1.

14. (Previously presented) The process of claim 11, wherein said L-amino-acid is selected from the group consisting of: L-asparagine; L-serine; L-glutamate; L-glycine; L-alanine; L-cysteine; L-valine; L-methionine; L-isoleucine; L-leucine; L-tyrosine; L-phenylalanine; L-histidine; L-lysine; L-tryptophan; and L-arginine.

15. (Previously presented) The process of claim 11, wherein said L-amino acid is L-threonine.
16. (Currently amended) The process of claim 11, wherein constituents of the fermentation broth and/or the biomass in its entirety or portions thereof remain in the isolated L-amino acid composition of step b).
17. (Currently amended) The process of claim 11, wherein said ~~modified~~ enterobacterium of the genus *Escherichia* further comprises ~~at least one overexpressed~~ one or more gene product products that are overexpressed, overexpression being achieved by increasing the copy number of the gene or genes or placing the gene or genes under the control of a strong promoter, compared to said enterobacterium prior to said overexpression the unmodified *Escherichia* and wherein the gene product is said one or more gene products are encoded by a gene or genes selected from the group consisting of:
 - a) ~~a *thrA* gene coding for aspartate kinase / homoserine dehydrogenase I an enzyme having the activity of both aspartate kinase and homoserine dehydrogenaseI;~~
 - b) a *thrB* gene coding for homoserine kinase;
 - c) a *thrC* gene coding for threonine synthase;
 - d) the *Corynebacterium glutamicum pyc* gene coding for pyruvate carboxylase;
 - e) a *pps* gene coding for phosphoenol pyruvate synthase;
 - f) a *ppc* gene coding for phosphoenol pyruvate carboxylase;
 - g) both the a *pntA* and a the *pntB* gene coding for the subunits of pyridine transhydrogenase;
 - h) the *Escherichia coli rhtB* gene coding for a protein imparting homoserine resistance;
 - i) a *mgo* gene coding for malate:quinone oxidoreductase;
 - j) the *Escherichia coli rhtC* gene coding for a protein imparting threonine resistance;
 - k) the *Corynebacterium glutamicum thrE* gene coding for a threonine export carrier protein;

- l) a *gdhA* gene encoding glutamate dehydrogenase;
- m) a *hns* gene encoding the DNA-binding protein HLP-II;
- n) a *pgm* gene encoding phosphoglucomutase;
- o) a *fba* gene encoding fructose ~~bisphosphate~~ bisphosphate aldolase;
- p) a *ptsH* gene encoding the phosphohistidine protein hexose phosphotransferase;
- q) a *ptsI* gene encoding enzyme I of the phosphotransferase system;
- r) a *crr* gene encoding the glucose-specific IIA component;
- s) a *ptsG* gene encoding the glucose-specific IIBC component;
- t) a *lrp* gene encoding the regulator of the leucine regulon;
- u) a *csrA* gene encoding the global regulator Csr;
- v) a *fadR* gene encoding the regulator of the fad regulon;
- w) a *iclR* gene encoding the regulator of central intermediate metabolism;
- x) a *mopB* gene encoding the 10 Kd chaperone;
- y) a an *ahpC* gene encoding the small subunit of alkyl hydroperoxide reductase;
- z) a an *ahpF* gene encoding the large subunit of alkyl hydroperoxide reductase;
- aa) a *cysK* gene encoding cysteine synthase A;
- bb) a *cysB* gene encoding the regulator of the cys regulon;
- cc) a *cysJ* gene encoding the flavoprotein of NADPH sulfite reductase;
- dd) a *cysI* gene encoding the haemoprotein of NADPH sulfite reductase;
- ee) a *cysH* gene encoding adenylyl sulfate reductase;
- ff) a *phoB* gene encoding the positive regulator PhoB of the pho regulon;
- gg) a *phoR* gene encoding the sensor protein of the pho regulon;
- hh) a *phoE* gene encoding protein E of the outer cell membrane;
- ii) a *pykF* gene which codes for fructose-stimulated pyruvate kinase I;
- jj) a *pfkB* gene encoding 6-phosphofructokinase II;
- kk) a *malE* gene encoding the periplasmic binding protein of maltose transport;
- ll) a *sodA* gene encoding superoxide dismutase;
- mm) a *rseA* gene encoding a protein with anti-sigmaE activity;

- nn) a rseC gene encoding a global regulator of the sigmaE factor;
 - oo) a sucA gene encoding the decarboxylase subunit of 2-ketoglutarate dehydrogenase;
 - pp) a sucB gene coding for the dihydrolipoyltranssuccinase E2 subunit of 2 ketoglutarate dehydrogenase;
 - qq) a sucC gene encoding the beta-subunit of succinyl-CoA synthetase;
 - rr) a sucD gene encoding the alpha-subunit of succinyl-CoA synthetase;
 - ss) a adk gene encoding adenylate kinase;
 - tt) a hdeA gene coding for a periplasmic protein with a chaperonin-like function;
 - uu) a hdeB gene which codes for a periplasmic protein with a chaperonin-like function;
 - vv) a icd gene coding for isocitrate dehydrogenase;
 - ww) a mglB gene coding for the periplasmic galactose-binding transport protein;
 - xx) a lpd gene coding for dihydrolipoamide dehydrogenase;
 - yy) a an aceE gene coding for the E1 component of the pyruvate dehydrogenase complex;
 - zz) a an aceF gene coding for the E2 component of the pyruvate dehydrogenase complex;
 - aaa) a pepB gene coding for aminopeptidase B;
 - bbb) a aldH gene coding for aldehyde dehydrogenase;
 - ccc) a bfr gene coding for the iron storage homoprotein;
 - ddd) a udp gene which codes for uridine phosphorylase; and
 - eee) a rseB gene which codes for the regulator of sigmaE factor activity.
18. (Currently amended) The process of claim 11, wherein said ~~modified~~ enterobacterium of the genus *Escherichia* further comprises at least one gene which is inactivated by one or more methods of mutagenesis selected from the group consisting of deletion of all or part of the gene, insertional mutagenesis due to homologous recombination, and transition or transversion mutagenesis with incorporation of a non-sense mutation in

the gene, compared to said enterobacterium ~~the unmodified *Escherichia*~~, prior to mutagenesis wherein the at least one gene is selected from the group consisting of:

- a) a *tdh* gene coding for threonine dehydrogenase;
- b) a *mdh* gene coding for malate dehydrogenase;
- c) the open reading frame (orf) *yjfA* of *E. coli*, when said modified *Escherichia* is *Escherichia coli*;
- d) the open reading frame (orf) *ytjP* of *E. coli*, when said modified *Escherichia* is *Escherichia coli*;
- e) a *pckA* gene coding for phosphoenol pyruvate carboxykinase;
- f) a *poxB* gene coding for pyruvate oxidase;
- g) an *aceA* gene coding for isocitrate lyase;
- h) a *dgsA* gene coding for the regulator DgsA of the phosphotransferase system;
- i) the *Escherichia coli fruR* gene coding for a fructose repressor;
- j) a *rpoS* gene which codes for the sigma³⁸ factor;
- k) an *aspA* gene encoding aspartate ammonium lyase; and
- l) an *aceB* gene encoding malate synthase A.

19. (Currently amended) The process of claim 11, wherein said ~~*Escherichia*~~ enterobacterium is of the species *Escherichia coli*.
20. (Previously presented) The process of claim 11, wherein the expression of the *yjgF* open reading frame has been eliminated by the deletion of part of the *yjgF* open reading frame.
21. (Previously presented) The process of claim 11, wherein the expression of the *yjgF* open reading frame has been eliminated by the deletion of all of the *yjgF* open reading frame.
22. (Currently amended) The process of claim 11, wherein said L-amino acid is recovered from ~~the modified *Escherichia*~~ said enterobacterium.

23. (Previously presented) The process of claim 11, wherein said L-amino acid is recovered from said medium.
24. (Previously presented) The process of claim 11, wherein culturing is continued until a maximum amount of the L-amino acid has been formed.
25. (Previously presented) The process of claim 11, wherein culturing is performed using a batch process.
26. (Previously presented) The process of claim 11, wherein culturing is performed using a fed batch process.
27. (Previously presented) The process of claim 11, wherein culturing is performed using a repeated fed batch process.